

COMPOSITIONS AND METHODS FOR ALTERING
AMINO ACID CONTENT OF PROTEINS

CROSS-REFERENCE TO RELATED APPLICATIONS

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5/7/02
This application claims the benefit of U.S. Application Serial No. 08/988,015,
filed December 10, 1997, ^{now abandoned} which is herein incorporated by reference.

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FIELD OF THE INVENTION

The invention relates to a process for the production of proteins having high
nutritional properties. The methods find particular use in the production of plants with
increased levels of amino acids having high nutritional properties through the
10 modification of plant genes.

BACKGROUND OF THE INVENTION

Autotrophic organisms can make all of their own amino acids. Other cells utilize
many preformed amino acids. Humans and other higher animals require a number of
15 essential amino acids in the diet. These essential amino acids are obtained directly or
indirectly by eating plants. These essential amino acids include lysine, tryptophan,
threonine, methionine, phenylalanine, leucine, valine and isoleucine.

Constructing proteins with higher nutritional value has been a long-sought goal of
scientists. Traditionally, agricultural scientists concentrated on breeding plants with high
20 nutritional yield. Typically, these new varieties were richer in carbohydrates but usually
poorer in essential proteins than the wild type varieties from which they were derived.

Seed storage proteins represent up to 90% of total seed protein in seeds of many plants. They are used as a source of nutrition for young seedlings in the period immediately following germination. The genes encoding them are strictly regulated, being expressed in a highly tissue specific and stage specific manner. These genes are almost exclusively expressed in developing seed. Different classes of seed storage proteins may be expressed at different stages in the development of the seed. They are typically stored in membrane bound organelles called protein bodies or protein storage vacuoles.

A related group of proteins, the vegetative storage proteins, have similar amino acid compositions and are also stored in specialized vacuoles. These proteins are generally found in leaves instead of seeds. These proteins are degraded upon flowering, and are thought to serve as a nutritive source for developing seeds.

Cereal grains and legume seeds which are key protein sources for the vegetarian diet are generally deficient in essential amino acids such as methionine, lysine, and threonine. Therefore, there is needed means for improving the nutritional quality of these proteins.

SUMMARY OF THE INVENTION

Compositions and methods for altering the amino acid profiles of proteins without introducing conformational changes into the protein are provided. The method involves preparing a binding partner and/or an interacting molecule which binds to the native protein and using such interacting molecule to select for modified proteins retaining the native conformation.

The method finds particular use in altering the nutritional value of proteins. A plant protein having increased methionine levels is provided. The modified protein retains the conformation of the native protein while having significantly higher levels of methionine.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows VSP homologies.

VSP-b (same as VSP β) and VSP-a (same as VSP α): Staswick, P.E., (1988), Plant Physiol. 87, 250-254.

T.phos (tomato acid phosphatase): Erion, J.L., Ballo, B., May, L., Bussell, J., Fox, T.W., & Thomas, S.R., SwissProt database accession number P27061.

Ph.vulg (Phaseolus vulgaris): Zhon, P-Y., Tanaka, T., Yamauchi, D., & Minamikawa, T. (1997), Plant Physiol. 113, 479-485.

Ar.VSP (Arabidopsis thaliana): Yu, D.Y., Quigley, F., & Mache, R., EMBL database accession number X79490.

Ar.1A-1, Ar.17A-1 (Arabidopsis thaliana, floral organs): Utsugi, S., Sakamoto, Ogura, Y., Murata, M., & Motoyoshi, F. (1996) Plant Mol. Biol. 32, 759-765.

Fig. 2 shows proposed VSP β methionine-enriched variants.

Fig. 3A shows the hydropathy index computation for sequence VSP β .

Fig. 3B shows the hydropathy index computation for sequence VSPMet10.

Fig. 3C shows the hydropathy index computation for sequence VSPMet20.

Fig. 3D shows the hydropathy index computation for sequence VSPMet30.

Fig. 4 shows the VSP β -met10 sequence.

Fig. 5 shows the colony lift assay to detect protein-protein interactions.

DETAILED DESCRIPTION OF THE INVENTION

Proteins having altered amino acid profiles are provided. The proteins can be designed to be enriched in essential amino acids, including lysine, methionine, tryptophan, threonine, phenylalanine, leucine, valine and isoleucine relative to average levels of such amino acids in the native protein.

Generally, knowledge of the three-dimensional (3-D) structure of a given protein allows one to engineer amino acid substitutions in a rational manner so as to effect a desired change in the property of the protein without compromising the folding process. The present invention provides methods for increasing the levels of essential amino acids within a protein while at the same time the altered protein has the conformation of the native protein.

The present invention provides methods for altering the amino acid content of a protein whose 3-D structure is unknown or unavailable. The method may also provide an easy method for assessing changes in a protein in which the structure of the protein is known but tools for confirming conformation of the protein may be unavailable. The "conformation" of a protein refers to the spatial arrangement of substituent groups of the molecule. The polypeptide chain of a protein has only one conformation (or a very few) under normal biological conditions of temperature and pH. This, referred to as the "native conformation," confers biological activity. The native conformation is sufficiently stable so that the protein can be isolated and retained in its native state. Therefore, it is important to be able to change the amino acid content of a protein, yet at the same time have the protein retain its biological activity.

The methods of the invention are useful for making amino acid changes within proteins whose conformation is unknown or unavailable. Such proteins include the vegetative storage protein which is believed to play a significant role in supplying amino acids for protein deposition during seed fill, and other proteins of the seed. The methods of the invention may be used to modify the amino acid composition of any protein. Examples of such proteins include but are not limited to wheat endosperm purothionine (Mak and Jones (1976) Can. J. Biochem. 22:83J); albumins (Higgins et al. (1986) J. Biol. Chem. 261:11124); and methionine rich proteins (Pedersen et al. (1986) J. Biol. Chem. 261:6279; Kirihaara et al. (1988) Gene 71:359; Musumura et al. (1989) Plant. Mol. Biol. 12:123).

The methods of the invention comprise altering the amino acid composition of a protein to produce an engineered protein. The engineered protein will retain the conformation and activity of the native protein yet have a modified or altered amino acid content. In this manner, levels of particular amino acids of interest can be increased or

decreased. Of particular interest, is to increase the levels or numbers of essential amino acids in the proteins. By essential amino acid is intended, lysine, tryptophan, threonine, methionine, phenylalanine, leucine, valine, isoleucine, and cysteine. However, it is recognized that the amino acid composition can be changed in various ways, as long as the changes do not affect the conformation of the final protein.

The proteins of the invention have been engineered or modified to contain altered amino acid levels. The engineered protein retains the conformation of the native protein. The method involves preparing binding partners and/or interacting molecules to the native protein and utilizing these interacting molecules to determine whether the engineered protein folds correctly. By "binding partner" or "interacting molecule" is intended a molecule which is capable of binding or interacting with the proteins of interest. Such binding partners or interacting molecules include antibodies, monoclonal antibodies, antibody fragments, proteins, modified proteins, nucleotide sequences, such as aptomers, chemical compounds (e.g. carbohydrates, etc.), or combinations thereof.

The interacting molecules also encompass polypeptides that have an intrinsic affinity to the protein of interest, particularly such polypeptides that are capable of binding with the protein of interest to form an oligomeric complex. For example, VSP-alpha binds VSP with high affinity and could be used as an interacting molecule for the altered VSP protein.

Methods for antibody production are known in the art. See, for example, *Antibodies, A Laboratory Manual*, Harlow and Lane (Eds.), Cold spring Harbor Laboratory Press, Coldspring Harbor, NY (1988), and the references cited therein. See also, Radka et al. (1983) *J. Immunol.* 128:2804; and Radka et al. (1984) *Immunogenetics* 19:63. All of which are herein incorporated by reference.

Once antibodies, preferably monoclonal antibodies, are available which bind to the native protein, such antibodies can be used to select for modified proteins which retain the conformation of the native protein. Strategies to identify residues within a protein that might tolerate amino acid substitution include mutational analysis, secondary structure prediction, homology comparison, and the like. Such strategies can be used to identify amino acids within the protein that will tolerate amino acid substitution.

By mutational analysis is intended mutagenic PCR and DNA shuffling. See, for example, Stemmer, W.P. (1994) Nature 370:389-391; and Stemmer, W.P. (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, herein incorporated by reference. Such methods can be used to generate phage display libraries of protein genes containing random mutations. Phage display is an in vitro selection technology which allows for a foreign protein or peptide to be displayed on the surface of filamentous phage, linking the phenotype of the phage to its genotype. Molecular repertoires with sufficient diversity can be generated using such technology. Proteins which exhibit the correct conformation, that is, the native conformation, can be selected for by the ability to bind antibodies recognizing conformational domains of the native protein. See also Methods in Enzymology, Combinatorial Chemistry, John N. Abelson (Ed.), Vol. 267, Academic Press, Inc., San Diego, CA, herein incorporated by reference. Once correctly-folded protein variants are determined, subsequent isolation and sequencing of the variants reveals the tolerated sites for mutations. Alternatively, correctly folded variants may be identified by other screening or selection methods such as filter lift-assay and ELISA.

Substitutions may also be incorporated at secondary structure prediction sites. Structural features of the protein are important for proper folding. Sequence analysis tools such as the GCG (Wisconsin sequence analysis package, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI) and PC/GENE (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, CA) can be used to analyze protein sequence for secondary structure features such as helices, sheets and turns. In this manner, it can be determined whether a particular stretch of amino acids may reside on the surface of the protein. Residues on the surface of a protein tolerate substitution more readily than buried residues without compromising the structure of the protein. Utilizing these algorithms, predicted turns and surface regions of the proteins can be made. Therefore, predictions can be made into which regions amino acid substitutions can be made without affecting conformation.

Sites for amino acid substitution can also be determined by homology comparison to other proteins. Nature has tested the tolerance of protein residues to substitution as exemplified in the sequences of proteins such as globins and cytochromes from several different species, members of which have the same fold. See, for example, Hampsey et

al. (1988) FEBS Lett. 231:275; Bashford et al. (1987) J. Mol. Biol. 196:199; Lesk and Chothia (1980) J. Mol. Biol. 136:225.

In designing proteins of the invention, hydrophobic residues, such as alanine, cysteine, valine, isoleucine, leucine, methionine, phenylalanine, and tryptophan may be substituted for one another without undue perturbation of the structure. Such residues generally occur in the hydrophobic core of the protein. See, Bowie et al. (1990) Science 247:1306-1310; and Baldwin and Matthews (1994) Curr. Opin. Biotech 5:396-402. See also Ladunga and Smith (1997) Prot. Eng. 10:187-196, herein incorporated by reference. Generally, residues that substitute for one another in related sequences do so by conserving the physico-chemical properties of the residue and folding of the protein thus conserving the 3-D structure of the protein.

Therefore, the protein to be modified can be compared with homologous proteins. Amino acids that are critical to the function and/or folding of the protein would be expected to be conserved over time. Therefore, predictions can be made as to which amino acids can be substituted without affecting the conformation or folding of the protein.

Such selected amino acid substitutions can be made by DNA sequencing, site-directed mutagenesis, or other methods which substitute one amino acid with any other amino acid.

Once the amino acid substitutions have been made and the conformation confirmed by antibody binding, the protein can be expressed using known expression systems. Where necessary, the DNA encoding the protein can be synthesized using known techniques. Likewise, the nucleotide sequence encoding the protein can be contained within expression cassettes.

Utilizing the methods of the invention, proteins can be constructed which have increased nutritional quality. That is, the essential amino acid content within the protein can be increased to represent at least about 5-about 10%, preferably at least about 10-about 20%, more preferably at least about 20-about 40% of the total amino acid content in the protein.

In the same manner, the amino acid content of a subject protein can be altered to include at least about 10% amino acid substitutions, additions or deletions, about 20% or

even up to about 30% to about 40%. It is recognized that the limitation will be the activity of the altered. The present invention provides a convenient and ready mechanism to test the activity of the protein by its ability to bind the interacting molecule.

For convenience for expression in plants, the nucleic acid encoding the modified peptides or proteins of the invention can be contained within expression cassettes. The expression cassette will comprise a transcriptional initiation region linked to the nucleic acid encoding the peptide of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene or genes of interest to be under the transcriptional regulation of the regulatory regions.

The transcriptional initiation region, the promoter, may be native or homologous or foreign or heterologous to the host, or could be the natural sequence or a synthetic sequence. By foreign is intended that the transcriptional initiation region is not found in the wild-type host into which the transcriptional initiation region is introduced.

15 ~~Sub G10~~ The transcriptional cassette will include the in 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., (1991) Mol. Gen. Genet. 262:141-144; Proudfoot (1991) Cell 64:671-674; Sanfacon et al. (1991) Genes Dev. 5:141-149; Mogen et al. (1990) Plant Cell 2:1261-1272; Munroe et al. (1990) Gene 91:151-158; Ballas et al. (1989) Nucleic Acids Res. 17:7891-7903; Joshi et al. (1987) Nucleic Acid Res. 15:9627-9639.

25 Where appropriate, the gene(s) expressing the modified proteins may be optimized for increased expression in the transformed plant. In this manner, the sequences can be synthesized using monocot, dicot or particular plant; i.e. maize, soybean, sorghum, wheat, etc., preferred codons for improved expression. Methods are available in the art for synthesizing plant preferred genes. See, for example, U.S. Patent
30 Nos. 5,380,831, 5,436, 391, and Murray et al. (1989) Nucleic Acids Res. 17:477-498, herein incorporated by reference.

The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein, O., Fuerst, T.R., and Moss, B. (1989) PNAS USA, 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al. (1986); MDMV leader (Maize Dwarf Mosaic Virus); Virology, 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP), (Macejak, D.G., and P. Sarnow (1991) Nature, 353:90-94; untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling, S.A., and Gehrke, L., (1987) Nature, 325:622-625; tobacco mosaic virus leader (TMV), (Gallie, D.R. et al. (1989) Molecular Biology of RNA, pages 237-256; and maize chlorotic mottle virus leader (MCMV) (Lommel, S.A. et al. (1991) Virology, 81:382-385). See also, Della-Cioppa et al. (1987) Plant Physiology, 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

The expression cassettes may contain one or more than one nucleic acid sequences to be transferred and expressed in the transformed plant. Thus, each nucleic acid sequence will be operably linked to 5' and 3' regulatory sequences. Alternatively, multiple expression cassettes may be provided.

Generally, the expression cassette will comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues. Such selectable marker genes are known in the art. See generally, G. T. Yarranton (1992) Curr. Opin. Biotech., 3:506-511; Christopherson et al. (1992) Proc. Natl. Acad. Sci. USA, 89:6314-6318; Yao et al. (1992) Cell, 71:63-72; W. S. Reznikoff (1992) Mol. Microbiol., 6:2419-2422; Barkley et al. (1980) The Operon, pp. 177-220; Hu et al. (1987) Cell, 48:555-566; Brown et al. (1987) Cell, 49:603-612; Figge et al. (1988) Cell, 52:713-722; Deuschle et al. (1989) Proc. Natl. Acad. Sci. USA, 86:5400-5404; Fuerst et al. (1989) Proc. Natl. Acad. Sci. USA, 86:2549-2553; Deuschle et al. (1990) Science, 248:480-483; M. Gossen (1993) PhD Thesis, University of Heidelberg; Reines et al. (1993) Proc. Natl. Acad. Sci. USA, 90:1917-1921; Labow et al. (1990) Mol. Cell Bio., 10:3343-3356; Zambretti et al. (1992) Proc. Natl. Acad. Sci. USA, 89:3952-3956; Baim et al. (1991) Proc. Natl. Acad. Sci. USA, 88:5072-5076; Wyborski

et al. (1991) *Nuc. Acids Res.*, 19:4647-4653; A. Hillenand-Wissman (1989) *Topics in Mol. and Struc. Biol.*, 10:143-162; Degenkolb et al. (1991) *Antimicrob. Agents Chemother.*, 35:1591-1595; Kleinschmidt et al. (1988) *Biochemistry*, 27:1094-1104; Gatz et al. (1992) *Plant J.*, 2:397-404; A. L. Bonin (1993) PhD Thesis, University of
5 Heidelberg; Gossen et al. (1992) *Proc. Natl. Acad. Sci. USA*, 89:5547-5551; Oliva et al. (1992) *Antimicrob. Agents Chemother.*, 36:913-919; Hlavka et al. (1985) *Handbook of Exp. Pharmacology*, 78; Gill et al. (1988) *Nature* 334:721-724; DeBlock et al. (1987) *EMBO J.*, 6:2513-2518; DeBlock et al. (1989) *Plant Physiol.*, 91:691-704; Fromm et al. (1990) 8:833-839; Gordon-Kamm et al. (1990) 2:603-618. Such disclosures are herein
10 incorporated by reference.

The nucleotide sequences of interest of this invention can be introduced into the genome of the desired host organism in a variety of techniques known in the art. For the purposes of this invention, it will be appreciated to those skilled in the art that any conventional transformation vector may be used as long as it is capable of transforming
15 the organism of choice and it does not have restriction sites in common with those comprising the final master insertion cassette. Hence, the detailed experimental description of transformation vectors is given by way of illustration only.

Vector systems are known for the transformation of yeast and bacterial cells. For yeast, these include but are not limited to autonomously replicating plasmids (see, for example, Stearns et al. (1990) *Methods Enzymol.* 185:280-297); 2-micron circle yeast
20 DNA sequences (see, for example, Hollenberg (1982) *Curr. Topics Microbiol. Immunol.* 96:119-144; Broach (1983) *Methods Enzymol.* 101:307-325; MacKay (1983) *Methods Enzymol.* 101:325-343; Armstrong (1989) *BioTechnology* 13:165-192; Rose (1990) *Methods Enzymol.* 185:234-279); linearized vector DNA (see, for example, see, for example, Takita et al. (1997) *Yeast* 13:763-768); artificial chromosome vectors (Burke (1987) *Science* 236:806-812); restriction site bank plasmids (Davison (1987), U.S. Patent No. 4,657,858, and *Methods Enzymol.* 153: 34-54); delta-integration vectors (see, for example, Lee and Da Silva (1997) *Biotechnol. Prog.* 13:368-373); and *Agrobacterium*-based vectors (see, for example, Bundock et al. (1995) *EMBO J.* 14:3206-3214; Piers et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:1613-1618; Risseuw et al. (1996) *Mol. Cell. Biol.* 16:5924-5932); and Shuttle Vectors (see, for example, Schneider (1991) *Methods*
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Enzymol 194:373-388; Singh (1997) Methods Mol. Biol. 62:113-130). See generally Hinnen (1980) Curr. Topics Microbiol. Immunol. 96:101-117; Nombela (1985) Revis. Biol. Cel. 4:1-25; Parent (1985) Yeast 1(2):83-138; West (1988) BioTechnology 10:387-404; Schena (1991) Methods Enzymol. 194:389-398; Schneider (1991) Methods
5 Enzymol. 194:373-388; and Singh (1997) Methods. Mol. Biol. 62:113-130.

Vector systems used for bacterial transformation include, but are not limited to, yeast shuttle vectors (see, for example, Ward (1990) Nucleic Acids Res. 18(17):5319; Strathern (1991) Methods Enzymol. 194:319-329; Soni (1992) Nucleic Acids Res. 20(21) 5852; Nacken (1994) Nucleic Acids Re. 22:1509-1510; Wehmeier (1995) Gene 165:149-
10 150); pBR322 and related plasmids such as pBR327 and pKC7 (see, for example, Rao and Rogers (1979) Gene 7:79-82; Talmadge and Gilbert (1980) Gene 12:235-241; Smith et al. (1995) Microbiology 141(pt. 1):181-188); pATH vectors (see, for example, Koerner et al. (1991) Methods in Enzymol. 194:477-490); yeast plasmids (see, for example, Marcil (1992) Nucleic Acids Res. 20:917); and natural replicon ColEI and related
15 plasmids such as P15A, F, RSF1010, and R616 (see, for example, Muhlenhoff and Chauvat (1996) Mol. Gen. Genet. 252:93-100; Sakai and Komano (1996) Biosci. Biotechnol. Biochem. 60:377-382; Lee and Henk (1997) Vet. Microbiol. 54:369-374); herein incorporated by reference.

A number of vector systems are also known for the introduction of foreign or
20 native genes into mammalian cells. These include SV40 virus (see, for example, Okayama et al. (1985) Molec. Cell. Biol. 5:1136-1142); Bovine papilloma virus (see, for example, DiMaio et al. (1982) Proc. Natl. Acad. Sci. USA 79:4030-4034); adenovirus (see, for example, Morin et al. (1987) Proc. Natl. Acad. Sci. USA 84:4626; Yifan et al. (1995) Proc. Natl. Acad. Sci. USA 92:1401-1405; Yang et al. (1996) Gene Ther. 3:137-
25 144; Tripathy et al. (1996) Nat. Med. 2:545-550; Quantin et al. (1992) Proc. Natl. Acad. Sci. USA 89:2581-2584; Rosenfeld et al. (1991) Science 252:431-434; Wagner (1992) Proc. Natl. Acad. Sci. USA 89:6099-6103; Curiel et al. (1992) Human Gene Therapy 3:147-154; Curiel (1991) Proc. Natl. Acad. Sci. USA 88:8850-8854; LeGal LaSalle et al. (1993) Science 259:590-599); Kass-Eisler et al. (1993) Proc. Natl. Acad. Sci. USA
30 90:11498-11502); adeno-associated virus (see, for example, Muzyczka et al. (1994) J. Clin. Invest. 94:1351; Xiao et al. (1996) J. Virol. 70:8098-8108); herpes simplex virus

(see, for example, Geller et al. (1988) *Science* 241:1667; Huard et al. (1995) *Gene Therapy* 2:385-392; U.S. Patent No. 5,501,979); retrovirus-based vectors (see, for example, Curran et al. (1982) *J. Virol.*, 44:674-682; Gazit et al. (1986) *J. Virol.*, 60:19-28; Miller (1992) *Curr. Top. Microbiol. Immunol.* 158:1-24; Cavanaugh et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:7071-7075; Smith et al. (1990) *Mol. Cell. Biol.* 10:3268-3271); herein incorporated by reference.

Methods of the present invention can be used to facilitate assembly of nucleotide sequences of interest for transformation of any plant. In this manner, genetically modified plants, plant cells, plant tissue, seed, and the like can be obtained. The transformation vector and hence method of transformation chosen will depend on the type of plant or plant cell, i.e. monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection (Crossway et al. (1986) *Biotechniques* 4:320-334); electroporation (Riggs et al. (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606); *Agrobacterium*-mediated transformation (Hinchee et al. (1988) *Biotechnology* 6:915-921); direct gene transfer (Paszkowski et al. (1984) *EMBO J.* 3:2717-2722); and ballistic particle acceleration (see, for example, Sanford et al. U.S. Patent 4,945,050; WO91/10725 and McCabe et al. (1988) *Biotechnology* 6:923-926). Also see, Weissinger et al. (1988) *Annual Rev. Genet.* 22:421-477; Sanford et al. (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou et al. (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe et al. (1988) *BioTechnology* 6:923-926 (soybean); Datta et al. (1990) *Biotechnology* 8:736-740 (rice); Klein et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein et al. (1988) *BioTechnology* 6:559-563 (maize); WO91/10725 (maize); Klein et al. (1988) *Plant Physiol.* 91:440-444 (maize); Fromm et al. (1990) *BioTechnology* 8:833-839; and Gordon-Kamm et al. (1990) *Plant Cell* 2:603-618 (maize); Hooydaas-Van Slogteren and Hooykaas (1984) *Nature (London)* 311:763-764; Bytebier et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet et al. (1985) *In The Experimental Manipulation of Ovule Tissues*, ed. G.P. Chapman et al., pp. 197-209 (Longman, N.Y.) (pollen); Kaeppler et al. (1990) *Plant Cell Reports* 9:415-418; and Kaeppler et al. (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin et al. (1992) *Plant Cell* 4:1495-1505 (electroporation); Li et al. (1993) *Plant Cell Reports* 12:250-255, and Christou and Ford (1995) *Annals of Botany*

compromise the VSP β structure may be good candidates for site-directed methionine substitutions.

In addition to this "random" approach, a method for the "semi-rational" incorporation of methionines into VSP was developed. Although the 3-D structure of VSP is uncertain, secondary structure prediction of the protein (see strategy 2 below) allowed "semi-rational" methionine substitutions. Analysis of VSP β homology with tomato acid phosphatase, a protein with 45% identity to VSP β , as well as other homologs allowed additional methionine substitutions (see strategy 3 below). Two methods were designed by which to introduce these substitutions. The first method involves DNA shuffling in the presence of excess methionine-encoding oligos which, by protein secondary structure predictions, are complementary to multiple regions of the VSP β gene corresponding to protein loops. The second novel method employed overlap PCR of segments of the VSP β gene corresponding to protein loops which have been amplified with the methionine-encoding oligos. The methods by which these oligos (corresponding to, for example, twenty-two different methionine substitutions) are introduced into VSP β result in the production of a library of phage-displayed VSP variants; theoretically each variant contains zero to twenty-two additional methionines. Subsequent phage display and biopanning of these libraries against VSP-specific monoclonal antibodies can lead to the identification of residues in VSP which can accommodate methionine without significantly altering the structure of the protein.

A VSP β mutant library was made by error prone PCR methodology (see below). From this pool of mutants, a filter lift assay (see methods) was performed to identify properly-folded mutant VSP β based on the ability to bind to either VSP α or a VSP-specific monoclonal antibody. Using VSP α as the antigen in a filter lift assay (Fig. 5) 18 out of 50 VSP β variants tested bound VSP α . Sequence analysis of 15 of these variants revealed a total of 84 point mutations which correlate with 58 AA substitutions and 25 silent mutations. Together these represent 51 different residues within the 218 AA VSP β .

2. Secondary structure prediction

Structural features of a protein are very important for proper folding. Sequence analysis tools such as the GCG (Wisconsin Sequence Analysis Package, Genetic

Computer Group, University Research Park, 575 Science Drive, Madison, WI) and PC/GENE (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, CA) were used to analyze the VSP β sequence for secondary structure features such as helices, sheets and turns and for determining whether a particular stretch of amino acids might reside on the surface of the protein. Residues on the surface of a protein would likely tolerate substitution more readily than a buried residue without compromising the structure of the protein. Using these algorithms, numerous predicted turns and surface regions of the protein were identified. Many of these regions are expected to tolerate methionine substitution. For example residues at positions 25, 30, 32, 37, 44, 65, 67, 102, 121, 130, 160, 163, 164, 169, 198, 202, and 207 in VSP β occur in predicted turn regions and were substituted with Met (Table 1).

3. Homology comparison

Over time, nature has tested the tolerance of protein residues to substitution, and this is exemplified in the sequences of proteins such as globins and cytochromes from several different species, members of which have the same fold (Hampsey, M.D., Das, G., Sherman, F. (1988) FEBS Lett. 231,275; Bashford, D., Chothia, C. & Lesk, A.M. (1987) J. Mol. Biol. 196, 199; Lesk, A.M. & Chothia, C. (1980) J. Mol. Biol. 136,225). These and other studies have demonstrated that hydrophobic residues (such as Ala, Val, Ile, Leu, Met, Phe and Trp) almost always occur in the hydrophobic core of the protein and that they may substitute for each other without undue perturbation of the structure (Bowie, J.U., Reidhaar-Olson, J.F., Lim, W.A., & Sauer, R.T. (1990) Science 247, 1306-1310; Baldwin, E.P., & Matthews, B.W. (1994) Curr. Opin. Biotech. 5, 396-402). Indeed, it has been observed that "Residue positions that can accept a number of different side chains, including charged and highly polar residues, are almost certain to be on the protein surface. Bowie et al. (1990) Science 247:1306-1310, have Residue positions that remain hydrophobic, whether variable or not, are likely to be buried within the structure". Furthermore, in a recent comprehensive analysis of substitution patterns in several databases of multiply aligned protein sequences, Ladunga and Smith (1997) Prot. Eng. 10:187-196, have concluded that the overall emphasis is on the preservation of three dimensional structure of the protein and that residues that substitute for each other

in related sequences do so by conserving the physico-chemical properties of the residue and the folding of the protein. In the case of VSP, this evolutionary data was utilized by comparing the homology of VSP β with six homologous proteins (Fig. 1). Amino acids that are critical to the function and/or folding of a protein would be expected to be conserved over time. For example, cysteine 7 and 29 are conserved in all seven of the homologous proteins aligned in Fig. 1. These residues are involved in forming a disulfide bond that may be expected to be of importance to the structure of the protein. In summary, analysis of the VSP β sequence with its homologs led to the identification of 31 residues (out of 218 amino acids) that in all likelihood will tolerate methionine substitution.

Engineering VSP β for increased methionine

Rational

Wild-type VSP β contains 1.4% methionine. Using the three strategies described, three different VSP β variants with increasing amounts of methionine have been proposed (9.6%, 14.2%, 17.9%, Fig. 2). The overall amino acid composition in each of these constructs is presented in Table 2. Construct VSP β -met20 (14.2% Met) contains the same 18 Met substitutions as the VSP β -met10 derivative plus an additional 11 Met residues. Likewise VSP β -met30 contains the same 29 Met substitutions as VSP β -met20 plus an additional 7 Met residues. Mutational analysis of VSP β resulted in the mutation of 51 different amino acids out of the 218 amino acid protein. Although these mutations were not methionine substitutions, the types of tolerated substitutions were examined for their relevance to substitution to a hydrophobic amino acid. For example, positions 50, 67, 93, 127, 150, and 164 tolerated mutation to a hydrophobic amino acid (Table 1). Therefore, it is possible that this same position might tolerate substitution to methionine. Positions 62, 67, 76, 127, and 164 are hydrophobic amino acids in VSP β - wild type. The observation that these positions tolerate substitution at all suggests they would more readily tolerate a conservative substitution (i.e., hydrophobic amino acid to hydrophobic amino acid, Table 1). Since residues 32, 50, 65, 67, 76, 93, 127, 150, 160, and 202 allowed non-conservative mutations, it is possible that these positions would tolerate mutation to methionine (Table 1). In every case where these amino acids were not

changed from or to a hydrophobic amino acid in the mutational analysis, at least one additional strategy (i.e., secondary structure or homology comparison) was used to rationalize methionine substitution at the particular position. In summary, in the three methionine enriched constructs proposed, 12 residues (out of a total of 36) were selected based at least in part on mutational analysis. More specifically, mutational analysis indicated 6/18 methionine substitutions in construct VSP β -met10, 9/29 in construct VSP β -met20, and 12/36 in VSP β -met30 (Table 1). As mentioned, mutational analysis revealed 51 different positions within VSP β tolerant to substitutions. Interestingly, 25/51 (49%) of the mutated positions are located in regions of the protein predicted to exist as turns, 17/51 (33%) in helices, and 9/51 (18%) in β -sheets. These percentages are significantly different from the predicted distribution of turns (25%), helices (25%) and β -sheets (50%), indicating that, as expected, the regions of the protein most likely to be located on the surface (e.g., turns) can more readily accommodate substitutions without compromising the structure of the protein. This suggests the importance of protein secondary structure prediction as one of the strategies utilized in the identification of residues for methionine substitution.

Since protein turns are generally more surface-exposed regions that do not contribute greatly to the overall structure of the protein, these regions were targeted for methionine substitution. In fact, out of the 36 positions selected for methionine substitution, 17 (47.2%) are predicted to occur in turns. In contrast, because β -sheets are protein structural elements that generally occur at the core of the protein, these regions were avoided in selecting sites for methionine substitution. Out of the 36 positions selected for methionine substitution, only 7 (19.4%) are predicted to occur in β -sheets. Nearly all of these residues were hydrophobic in wild-type VSP β and were thought to tolerate methionine based upon the homology comparison strategy. Additionally, 12 (33.3%) of the residues selected for methionine substitution in the three constructs are predicted to occur in helices. In summary, secondary structure prediction is the strategy responsible, at least in part, for 17/36 sites targeted for methionine substitution. More specifically, secondary structure prediction correlates with the selection of 7/18, 14/29, and 17/36 amino acids for methionine substitution in constructs VSP β -met10, VSP β -met20, and VSP β -met30, respectively (Table 1).

Homology comparison was a very informative strategy in selecting residues that might tolerate methionine substitution. Accordingly, methionine substitutions in VSPβ were made by adhering to the following rules and also summarized in Table 1:

Sub G11
5 (a) Conserved residues (highlighted in blue in Fig. 1) were defined as those residues occurring in more than 5 of the 7 homologs. These were not targeted for substitution. The exceptions were: at residue numbers 19, 37, 146 and 179 (one of the homologs contained a methionine residue); at positions 67, 80, 130 and 169 (conserved hydrophobic amino acid exchanges observed in at least one sequence) and at position 50 (non-conservative changes from Asn to Ser/Cys in two sequences).

10 (b) Similarly, non-conserved positions were defined as those containing residues with different side-chain properties. Several positions in VSPβ were correlated with non-conservative amino acids in the homologs (e.g., 5, 19, 25, 30, 37, 44, 60, 62, 65, 67, 72, 76, 80, 90, 97, 102, 121, 127, 130, 135, 142, 146, 150, 164, 169, 179, 189, 198, 202, 207, and 217). Such residues likely reside on the surface/turns of the protein and
15 were considered less important for protein function and/or folding and therefore targeted for substitution with methionine.

(c) In addition, some positions in which at least one other hydrophobic amino acid was observed among homologs (e.g., 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 25, 30, 37, 44, 60, 62, 65, 67, 72, 76, 90, and 97) were also expected to
20 tolerate substitution to the hydrophobic amino acid methionine. Exceptions to this were cases in which the hydrophobic amino acid was completely conserved in all 6 homologs (e.g., Val 49, Leu 77, Leu 110, Leu 114, Leu 145, Ile 157, Leu 158, Ile 186, Val 187, Leu 197 and Leu 210). In these cases, the possibility that the specific hydrophobic amino acid in the wild-type protein may be playing a role critical for the proper structure and/or
25 function of the protein was considered. To avoid disturbing this possible role, the substitution of any residue that is completely conserved in all 6 homologs examined was not proposed.

(d) Six residues within VSPβ that were expected to tolerate methionine substitution were identified based on the presence of methionine in analogous positions in
30 homologs (e.g., 19, 37, 44, 146, 179, and 202).

A few additional considerations were observed in selecting amino acids that might tolerate methionine substitution.

(e) We avoided altering histidine residues due to their potential importance in phosphatase activity of VSP β (Table 2 and DeWald, D.B., Mason, H.S., & Mullet, J.E. (1992) J. Biol. Chem. 267, 15958-15964).

(f) Since VSP β is a glycoprotein, this feature may be important for the stability and/or function of the protein, substitution of potential glycosylation sites was avoided (e.g., Asn 94).

(g) In addition, wherever possible, charged residues such as Lys, Arg, Glx, Asx were left untouched to preserve the hydrophobic/hydrophilic balance of the protein (Table 2 and Fig. 3A-D). While wild-type VSP β has a calculated charge of -4, VSP β -met10, VSP β -met20, and VSP β -met30 have calculated charges of -7, -7, and -5, respectively.

As a strategy, homology comparison facilitated, at least in part, the selection of 31/36 of the residues proposed for methionine substitution. These selections correlate with 18/18, 28/29, and 31/36 residues for constructs VSP β -met10, VSP β -met20, and VSP β -met30, respectively (Table 1).

Several of the amino acids selected for methionine substitution in the three constructs resulted from more than one strategy. In fact, the majority (20/36) of the targeted residues resulted from at least two strategies, with a few (4/36) resulting from all three strategies.

Experimental results

A synthetic gene for methionine enriched VSP β -met10 has been constructed. This synthetic gene differs from wild-type VSP β in that it encodes eighteen additional methionines (Fig. 4). Also, a few silent point mutations were introduced into this construct to create unique restriction sites. To test whether the proposed VSP β -met10 gene was correctly folded, the construct was cloned into the phagemid vector pCANTAB-5E and the abilities of the expressed proteins to bind VSP-specific conformational monoclonal antibodies in a filter lift assay were compared. The results indicate that the VSP β -met10 gene was able to bind the same antibodies as wild-type

VSP β . This suggests that VSP β -met10 may be correctly folded in an E. coli secretion system.

Together, these interdisciplinary approaches should not only result in the engineering of a nutritionally-enhanced VSP, but also provide clues to the structure of

- 5 VSP - a protein for which no 3D structure is available. This approach is applicable to any protein of interest.

Methods

1. Random mutation of vegetative storage protein (VSP β) by error-prone PCR

- 10 The VSP β gene was amplified by mutagenic PCR using primers flanking the gene.

<u>Reaction 1</u>	<u>Reaction 2</u>	<u>Reaction 3</u>	<u>Reaction 4</u>
10mM Tris-HCl	10mM Tris-HCl	10mM Tris-HCl	10mM Tris-HCl
50mM KCl	50mM KCl	50mM KCl	50mM KCl
9.5mM MgCl ₂	9.mM mgCl ₂	9.mM mgCl ₂	9.mM mgCl ₂
0.5mM MnCl ₂	0.5mM MnCl ₂	0.5mM MnCl ₂	0.5mM MnCl ₂
5 μ g/ml BSA	5 μ g/ml BSA	5 μ g/ml BSA	5 μ g/ml BSA
600pmol VSP template	600pmol VSP template	600pmol VSP template	600pmol VSP template
0.1 μ m each primer	0.1 μ m each primer	0.1 μ m each primer	0.1 μ m each primer
2mM dATP	200 μ M dATP	200 μ M dATP	200 μ M dATP
200 μ M dCTP	2mM dCTP	200 μ M dCTP	200 μ M dCTP
200 μ M dGTP	200 μ M dGTP	2mM dGTP	200 μ M dGTP
200 μ M dTTP	200 μ M dTTP	200 μ M dTTP	2mM dTTP
2 Units Taq Pol	2 Units Taq Po	2 Units Taq Pol	2 Units Taq Pol

1 cycle (1 min. at 95°C, 1 min. at 51°C, 3 min. at 72°C)

16 cycles (1 min. at 91°C, 1 min. at 51°C, 3 min. at 72°C)

- 15 1 cycle (1 min. a 91°C, 1 min. at 51°C, 5 min. at 72°C)

The products of these four reactions were pooled, and the band corresponding to the mutagenized VSP β gene was purified from an agarose gel, digested with SfiI and NotI and cloned into the phagemid vector pCANTAB-5E.

5 2. Filter lift assay

Sub 612
Fifty E. coli colonies containing randomly mutated VSP β genes were picked as small patches to an SB agar plate containing glucose and ampicillin. Patches were allowed to grow overnight at 37°C and were then transferred to a nitrocellulose filter. On the surface of an SB agar plate containing ampicillin and IPTG, this filter was placed on top (cell-side up) of a separate blocked filter to which the antigen (e.g., VSP α) had been coated. During an overnight incubation at 30°C, the cells expressed the VSP β variant they encoded. These proteins were able to diffuse through the top filter and, if correctly folded, bind the antigen-coated filter below. The next day, the antigen-coated filter was washed with PBS-0.05% tween and incubated with HRP/anti-e tag conjugate. Since the VSP β mutants are cloned into the pCANTAB-5E vector which fuses a C-terminal epitope tag (e-tag) to the VSP β protein variants, bound proteins were detected by this antibody in combination with enhanced chemiluminescence detection.

Table 1
Proposed Methionine Substitutions

Homology Comparison						
VSPβ position		Mutational Analysis ¹	Secondary Structure ²	Original A. A. hyrophobic?	Met in homolog? ³	# homologs hydrophobic ⁴
Construct 1 (9.6% Met)						
5	Y	-	-	Y	-	3 of 6
19	I	-	-	Y	Y-Ar. VSP	6 of 6
30	V	-	T	Y	-	2 of 6
37	I	-	T	Y	Y-T. phos	6 of 6
44	I	-	T	Y	Y-T. phos	1 of 6
60	R	-	-	-	-	5 of 6
62	V	V-A	-	Y	-	6 of 6
67	I	I-T, L	T	Y	-	5 of 6
72	I	-	-	Y	-	6 of 6
76	V	V-G	-	Y	-	5 of 6
121	L	-	T	Y	-	6 of 6
127	I	I-T, L	-	Y	-	3 of 6
146	K	-	-	-	Y-T. phos	1 of 6
164	I	I-V	T	Y	-	3 of 5
179	L	-	-	Y	Y-T. phos	6 of 6
189	I	-	-	Y	-	2 of 6
202	R	R-G, T	T	-	Y-T. phos	1 of 6
217	I	-	-	Y	-	5 of 6
Construct 2-additonal substitutions (14.7% Met)						
32	P	P-Q	T	-	-	0 of 6
65	N	N-S	T	-	-	3 of 6
90	V	-	-	Y	-	2 of 6
97	L	-	-	Y	-	1 of 6
102	V	-	T	Y	-	5 of 6
130	L	-	T	Y	-	6 of 6
135	L	-	-	Y	-	1 of 5
150	F	F-S, I, L	-	-	-	3 of 6
169	L	-	T	Y	-	5 of 6
198	T	-	T	-	-	5 of 6
207	T	-	T	-	-	3 of 6
Construct 3-additonal substitutions (17.9% Met)						
25	I	-	T	Y	-	6 of 6
50	N	N-I	-	-	-	0 of 6
80	I	-	-	Y	-	6 of 6
93	F	F-V	-	-	-	0 of 6
142	E	-	-	-	-	3 of 6
160	D	D-Y	T	-	-	0 of 6
163	L	-	T	Y	-	0 of 6

¹ Amino acid substitution observed in the mutational analysis. For example, at position 62, a valine to alanine substitution was observed.

² "T" indicates turn predicted by secondary structure analysis of VSPβ.

³ "Y" indicates the presence of Methionine in the designated VSP homolog.

⁴ Includes only aliphatic hydrophobic amino acids such as Leu, Ile, Val, and Met.

Table 2

Amino Acid Composition of VSP β -WT and Methionine-Enriched Variants

	VSP β	VSP β -Met10	VSP β -Met20	VSP β -Met30
Ala	13	13	13	13
Arg	11	9	9	9
Asn	14	14	13	12
Asp	11	11	11	10
Cys	2	2	2	2
Gln	6	6	6	6
Glu	19	19	19	18
Gly	13	13	13	13
His	7	7	7	7
Ile	14	6	6	4
Leu	20	18	13	12
Lys	15	14	14	14
MET	3 (1.4%)	21 (9.6%)	32 (14.7%)	39 (17.9%)
Phe	12	12	11	10
Pro	9	9	8	8
Ser	13	12	12	12
Thr	10	10	9	9
Trp	3	3	3	3
Tyr	12	12	12	12
Val	11	7	5	5
Total	218	218	218	218

5

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

10

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.